

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ceriani, Roberto L.
Peterson, Jerry A.
Larocca, David J.
- (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON
HMFG DIFFERENTIATION ANTIGEN
BINDING SPECIFICITY, COMPOSITION,
KIT & METHODS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Ratner & Prestia
(B) STREET: Suite 301
One Westlakes, Berwyn
(C) CITY: Valley Forge
(D) STATE: Pennsylvania
(E) COUNTRY: USA
(F) ZIP: 19482
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk 3.5"
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
(D) SOFTWARE: PatentIn #1.0,
Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: January 2, 2002
(C) CLASSIFICATION:

PARENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/482,596
(B) FILING DATE: June 7, 1995
(C) CLASSIFICATION:

grand parent APPLICATION DATA:
(A) APPLICATION NUMBER: 07/607,538
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Amzel, Viviana
(B) REGISTRATION No.: 30,930
(C) REFERENCE/DOCKET No: CRFC-047
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (610) 407-0700

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(C) TELEX: N.A.

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50
100
150
200
250
300
350
400
450
500
550
600
650
700
750
800
850
900
950
1000
1050
1100
1150
1200
1250
1300
1350
1384

GATTTTCATCC ATGATGTTAA TAAAAAACAC AAGGAGTTTG TGGGTAAGTCTG
GAACAAAAAC GCGGTGCATG TCAACCTGTT TGAGACCCCT GTGGAGGCTC
AGTACGTGAG ATTGTACCCC ACGAGCTGCC ACACGGCCTG CACTCTGCGC
TTTGAGCTAC TGGGCTGTGA GCTGAACGGA TGCGCCAATC CCCTGGGCTC
GAAGAATAAC AGCATCCCTG ACAAGCAGAT CACGGCCTCC AGCAGCTACA
AGACCTGGGG CTTGCATCTC TTCAGCTGGA ACCCTCCTA TGCACGGCTG
GACAAGCAGG GCAACTTCAA CGCCTGGGTT GCGGGGAGCT ACGGTAACGA
TCAGTGGCTG CAGGTGGACC TGGGCTCCTC GAAGGAGGTG ACAGGCATCA
TCACCCAGGG GGCCCGTAAC TTTGGCTCTG TCCAGTTTGT GGCATCCTAC
AAGGTTGCCT ACAGTAATGA CAGTGCGAAC TGGACTGAGT ACCAGGACCC
CAGGACTGGC AGCAGTAAGA TCTTCCCTGG CAACTGGGAC AACCCTCCC
ACAAGAAGAA CTTGTTTGAG ACGCCCATCC TGGCTCGCTA TGTGCGCATC
CTGCCTGTAG CCTGGCACAA CCGCATCGCC CTGCGCCTGG AGCTGCTGGG
CTGTTAGTGG CCACCTGCCA CCCCAGGTC TTCCTGCTTT CCATGGGCCC
GCTGCCTCTT GGCTTCTCAG CCCCTTTAAA TCACCATAGG GCTGGGGACT
GGGGAAGGGG AGGGTGTTC AAGGCAGCAC CACCACACAG TCACCCCTCC
CTCCCTCTTT CCCACCTCC ACCTCTCAG GGCCTGCCC CAGCCCTAA
GCCCCGTCCC CTAACCCCA GTCCCTCACTG TCCTGTTTTT TTAGGCACTG
AGGGATCTGA GTAGGTCTGG GATGGACAGG AAAGGGCAAA GTAGGGCGTG
TGGTTTCCCT GCCCTGTCC GGACCGCCGA TCCCAGGTGC GTGTGTCTCT
TGCTCTCCTA GCCCTCTCT CACACATCAC ATTCCCATGG TGGCTCAAG
AAAGGCCCGG AAGCCCCAGG CTGGAGATAA CAGCCTCTTG CCCGTCGGCC
CTGCGTCGGC CCTGGGGTAC CATGTGCCAC AACTGCTGTG GCCCCCTGTC
CCCAAGACAC TTCCCTTGT CTCCCTGGTT GCCTCTCTTG CCCCTTGTCC
TGAAGCCCAG CGACACAGAA GGGGGTGGGG CGGGTCTATG GGGAGAAAGG
GAGCGAGGTC AGAGGAGGGC ATGGGTGGC AGGGTGGGCG TTTGGGGCCC
TCATGTGGC TTTTCACCCC AGAGGACACA GGCAGCTTCC AAAATATATT
TATCTTCTTC ACGGGAAAAA AAAAAAAAAA ACCG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val
 1 5 10
 Gly Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu
 15 20 25
 Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser
 30 35 40
 Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys
 45 50 55
 Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn
 60 65 70
 Ser Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys
 75 80
 Thr Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala
 85 90 95
 Arg Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly
 100 105 110
 Ser Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser
 115 120 125
 Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn
 130 135 140
 Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr
 145 150
 Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
 155 160 165
 Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His
 170 175 180
 Ser His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg
 185 190 195
 Tyr Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala
 200 205 210
 Leu Arg Leu Glu Leu Leu Gly Cys
 215

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val Gly
 1 5 10
 Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu Thr
 15 20 25
 Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser Cys
 30 35 40
 His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu
 45 50 55
 Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser
 60 65 70
 Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr
 75 80
 Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg
 85 90 95
 Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly Ser

100						105						110		
Tyr	Gly	Asn	Asp	Gln	Trp	Leu	Gln	Val	Asp	Leu	Gly	Ser	Ser	
		115					120					120		
Lys	Glu	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asn	Phe	
			130					135					140	
Gly	Ser	Val	Gln	Phe	Val	Ala	Ser	Tyr	Lys	Val	Ala	Tyr	Ser	
			145						150					
Asn	Asp	Ser	Ala	Asn	Trp	Thr	Glu	Tyr	Gln	Asp	Pro	Arg	Thr	
155					160					165				
Gly	Ser	Ser	Lys	Ile	Phe	Pro	Gly	Asn	Trp	Asp	Asn	His	Ser	
	170					175					180			
His	Lys	Lys	Asn	Leu	Phe	Glu	Thr	Pro	Ile	Leu	Ala	Arg	Tyr	
	185					190					195			
Val	Arg	Ile	Leu	Pro	Val	Ala	Trp	His	Asn	Arg	Ile	Ala	Leu	
		200						205				210		
Arg	Leu	Glu	Leu	Leu	Gly	Cys								
			215		217									

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

32

Phe	Lys	Gly	Asn	Ser	Thr	Arg	Asn	Val	Met	Tyr	Phe	Asn	Gly
1				5					10				
Asn	Ser	Asp	Ala	Ser	Thr	Ile	Lys	Glu	Asn	Gln	Phe	Asp	Pro
15				20					25				
Pro	Ile	Val	Ala	Arg	Tyr	Ile	Arg	Ile	Ser	Pro	Thr	Arg	Ala
	30					35				40			
Tyr	Asn	Arg	Pro	Thr	Leu	Arg	Leu	Glu	Leu	Gln	Gly	Cys	Glu
	45					50				55			
Val	Asn	Gly	Cys	Ser	Thr	Pro	Leu	Gly	Met	Glu	Asn	Gly	Lys
	60					65				70			
Ile	Glu	Asn	Lys	Gln	Ile	Thr	Ala	Ser	Phe	Lys	Lys	Ser	
	75					80							
Trp	Trp	Gly	Asp	Tyr	Trp	Glu	Pro	Phe	Arg	Ala	Arg	Leu	Asn
85				90					95				
Ala	Gln	Gly	Arg	Val	Asn	Ala	Trp	Gln	Ala	Lys	Ala	Asn	Asn
100					105				110				
Asn	Lys	Gln	Trp	Leu	Glu	Ile	Asp	Leu	Leu	Lys	Ile	Lys	Lys
	115					120				125			
Ile	Thr	Ala	Ile	Ile	Thr	Gln	Gly	Cys	Lys	Ser	Leu	Ser	Ser
	130					135				140			
Glu	Met	Tyr	Val	Lys	Ser	Tyr	Thr	Ile	His	Tyr	Ser	Glu	Gln
	145					150							
Gly	Val	Glu	Trp	Lys	Pro	Tyr	Arg	Leu	Lys	Ser	Ser	Met	Val
155				160					165				
Asp	Lys	Ile	Phe	Glu	Gly	Asn	Thr	Asn	Thr	Lys	Gly	His	Val
	170				175				180				
Lys	Asn	Phe	Phe	Asn	Pro	Pro	Ile	Ile	Ser	Arg	Phe	Ile	Arg
	185					190				195			
Val	Ile	Pro	Lys	Thr	Trp	Asn	Gln	Ser	Ile	Ala	Leu	Arg	Leu
	200					205					210		

Glu Leu Phe Gly Cys Asp Ile Tyr
215 218

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly
1 5 10
Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro
15 20 25
Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr
30 35 40
Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp
45 50 55
Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala
60 65 70
Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn
75 80
Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu
85 90 95
Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro
100 105 110
Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val
115 120 125
Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Glu
130 135 140
Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly
145 150
His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val
155 160 165
Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser
170 175 180
Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro
185 190 195
Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu
200 205 210
Gly Cys Glu Ala Gln Asp Leu Tyr
215 218